

SEQUENCE LISTING

<110> POELLINGER, Lorenz

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RUAS, Jorge

<120> MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE
FACTOR-1 BY THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN

<130> 3743/49008

<150> US 60/223,480

<151> 2000-08-07

<160> 7

<170> PatentIn version 3.0

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(639)

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gag	gca	ggc	gtc	gaa	gag	tac	ggc	cct	gaa	gaa	gac	ggc	ggg	gag	gag	96
Glu	Ala	Gly	Val	Glu	Glu	Tyr	Gly	Pro	Glu	Glu	Asp	Gly	Gly	Glu	Glu	
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tcg	ggc	gcc	gag	gag	tcc	ggc	ccg	gaa	gag	tcc	ggc	ccg	gag	gaa	ctg	144
Ser	Gly	Ala	Glu	Glu	Ser	Gly	Pro	Glu	Glu	Ser	Gly	Pro	Glu	Glu	Leu	
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ggc	gcc	gag	gag	gag	atg	gag	gcc	ggg	cgg	ccg	cgg	ccc	gtg	ctg	cgc	192
Gly	Ala	Glu	Glu	Glu	Met	Glu	Ala	Gly	Arg	Pro	Arg	Pro	Val	Leu	Arg	
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09922958-080701

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ccg cgc gtc gtg ctg ccc gta tgg ctc aac ttc gac ggc gag ccg cag Pro Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln 85 90 95	288
ccc tac cca acg ctg ccg cct ggc acg ggc cgc cgc atc cac agc tac Pro Tyr Pro Thr Leu Pro Pro Gly Thr 105 100 110	336
cga ggt cac ctt tgg ctc ttc aga gat gca ggg aca cac gat ggg ctt Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu 115 120 125	384
ctg gtt aac caa act gaa tta ttt gtg cca tct ctc aat gtt gac gga Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly 130 135 140	432
cag cct att ttt gcc aat atc aca ctg cca gtg tat act ctg aaa gag Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val Tyr Thr Leu Lys Glu 145 150 155 160	480
cga tgc ctc cag gtt gtc cgg agc cta gtc aag cct gag aat tac agg Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg 165 170 175	528
aga ctg gac atc gtc agg tcg ctc tac gaa gat ctg gaa gac cac cca Arg Leu Asp Ile Val Arg Ser Leu Tyr Glu Asp Leu Glu Asp His Pro 180 185 190	576
aat gtg cag aaa gac ctg gag cgg ctg aca cag gag cgc att gca cat Asn Val Gln Lys Asp Leu Glu Arg Leu Thr Gln Glu Arg Ile Ala His 195 200 205	624
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<212> PRT

<213> Homo sapiens

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Ser	Gly	Ala	Glu	Glu	Ser	Gly	Pro	Glu	Glu	Ser	Gly	Pro	Glu	Glu	Leu
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Gly Ala Glu Glu Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg
50 55 60

Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn Arg Ser
65 70 75 80

Pro Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln
85 90 95

Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His Ser Tyr
100 105 110

Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu
115 120 125

Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly
130 135 140

Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val Tyr Thr Leu Lys Glu
145 150 155 160

Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg
165 170 175

Arg Leu Asp Ile Val Arg Ser Leu Tyr Glu Asp Leu Glu Asp His Pro
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<221> CDS

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Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
20 25 30

gaa tct gaa gtt ttt tat gag ctt gct cat cag ttg cca ctt cca cat 144
Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
35 40 45

aat gtg agt tcg cat ctt gat aag gcc tct gtg atg agg ctt acc atc 192
Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
50 55 60

agc tat ttg cgt gtg agg aaa ctt ctg gat gct ggt gat ttg gat att 240
Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
65 70 75 80

gaa gat gac atg aaa gca cag atg aat tgc ttt tat ttg aaa gcc ttg 288
Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
85 90 95

gat ggt ttt gtt atg gtt ctc aca gat gat ggt gac atg att tac att 336
Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
100 105 110

tct gat aat gtg aac aaa tac atg gga tta act cag ttt gaa cta act 384
Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
115 120 125

gga cac agt gtg ttt gat ttt act cat cca tgt gac cat gag gaa atg 432
Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
130 135 140

aga gaa atg ctt aca cac aga aat ggc ctt gtg aaa aag ggt aaa gaa 480
Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
145 150 155 160

caa aac aca cag cga agc ttt ttt ctc aga atg aag tgt acc cta act 528
Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
165 170 175

agc cga gga aga act atg aac ata aag tct gca aca tgg aag gta ttg 576
Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
180 185 190

cac tgc aca ggc cac att cac gta tat gat acc aac agt aac caa cct 624
His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
195 200 205

cag tgt ggg tat aag aaa cca cct atg acc tgc ttg gtg ctg att tgt 672
Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
210 215 220

gaa ccc att cct cac cca tca aat att gaa att cct tta gat agc aag 720
Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
225 230 235 240

act ttc ctc agt cga cac agc ctg gat atg aaa ttt tct tat tgt gat 768
Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp

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cgc Arg	tca Ser	att Ile 275	tat Tyr	gaa Glu	tat Tyr	tat Tyr	cat His 280	gct Ala	ttg Leu	gac Asp	tct Ser	gat Asp 285	cat His	ctg Leu	acc Thr	864			
aaa Lys	act Thr 290	cat His	cat His	gat Asp	atg Met	ttt Phe 295	act Thr	aaa Lys	gga Gly	caa Gln	gtc Val 300	acc Thr	aca Thr	gga Gly	cag Gln	912			
tac Tyr 305	agg Arg	atg Met	ctt Leu	gcc Ala 310	aaa Lys	aga Arg	ggt Gly	gga Gly	tat Tyr	gtc Val 315	tgg Trp	gtt Val	gaa Glu	act Thr	caa Gln 320	960			
gca Ala	act Thr	gtc Val	ata Ile 325	tat Tyr	aac Asn	acc Thr	aag Lys	aat Asn 330	tct Ser	caa Gln	cca Pro	cag Gln	tgc Cys	att Ile 335	gta Val	1008			
tgt Cys	gtg Val	aat Asn 340	tac Tyr	gtt Val	gtg Val	agt Ser	ggt Gly	att Ile 345	att Ile	cag Gln	cac His	gac Asp 350	ttg Leu	att Ile	ttc Phe	1056			
tcc Ser	ctt Leu	caa Gln 355	caa Gln	aca Thr	gaa Glu	tgt Cys	gtc Val 360	ctt Leu	aaa Lys	ccg Pro	gtt Val 365	gaa Glu	tct Ser	tca Ser	gat Asp	1104			
atg Met	aaa Lys 370	atg Met	act Thr	cag Gln	cta Leu	ttc Phe 375	acc Thr	aaa Lys	gtt Val	gaa Glu	tca Ser 380	gaa Glu	gat Asp	aca Thr	agt Ser	1152			
agc Ser 385	ctc Leu	ttt Phe	gac Asp	aaa Lys	ctt Leu 390	aag Lys	aag Lys	gaa Glu	cct Pro	gat Asp 395	gct Ala	tta Leu	act Thr	ttg Leu	ctg Leu 400	1200			
gcc Ala	cca Pro	gcc Ala	gct Ala 405	gga Gly	gac Asp	aca Thr	atc Ile	ata Ile 410	tct Ser	tta Leu	gat Asp	ttt Phe	ggc Gly 415	agc Ser	aac Asn	1248			
gac Asp	aca Thr	gaa Glu	act Thr 420	gat Asp	gac Asp	cag Gln	caa Gln	ctt Leu 425	gag Glu	gaa Glu	gta Val	cca Pro	tta Leu 430	tat Tyr	aat Asn	1296			
gat Asp	gta Val	atg Met 435	ctc Leu	ccc Pro	tca Ser	ccc Pro	aac Asn 440	gaa Glu	aaa Lys	tta Leu	cag Gln	aat Asn 445	ata Ile	aat Asn	ttg Leu	1344			
gca Ala	atg Met 450	tct Ser	cca Pro	tta Leu	ccc Pro	acc Thr 455	gct Ala	gaa Glu	acg Thr	cca Pro	aag Lys 460	cca Pro	ctt Leu	cga Arg	agt Ser	1392			
agt Ser 465	gct Ala	gac Asp	cct Pro	gca Ala	ctc Leu 470	aat Asn	caa Gln	gaa Glu	gtt Val	gca Ala 475	tta Leu	aaa Lys	tta Leu	gaa Glu	cca Pro 480	1440			
aat Asn	cca Pro	gag Glu	tca Ser 485	ctg Leu	gaa Glu	ctt Leu	tct Ser	ttt Phe 490	acc Thr	atg Met	ccc Pro	cag Gln	att Ile 495	cag Gln	gat Asp	1488			
cag	aca	cct	agt	cct	tcc	gat	gga	agc	act	aga	caa	agt	tca	cct	gag	1536			

Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu	
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cct aat agt ccc agt gaa tat tgt ttt tat gtg gat agt gat atg gtc	1584
Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val	
515 520 525	
aat gaa ttc aag ttg gaa ttg gta gaa aaa ctt ttt gct gaa gac aca	1632
Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr	
530 535 540	
gaa gca aag aac cca ttt tct act cag gac aca gat tta gac ttg gag	1680
Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu	
545 550 555 560	
atg tta gct ccc tat atc cca atg gat gat gac ttc cag tta cgt tcc	1728
Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser	
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Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser	
580 585 590	
gca agt cct caa agc aca gtt aca gta ttc cag cag act caa ata caa	1824
Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln	
595 600 605	
gaa cct act gct aat gcc acc act acc act gcc acc act gat gaa tta	1872
Glu Pro Thr Ala Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu	
610 615 620	
aaa aca gtg aca aaa gac cgt atg gaa gac att aaa ata ttg att gca	1920
Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala	
625 630 635 640	
tct cca tct cct acc cac ata cat aaa gaa act act agt gcc aca tca	1968
Ser Pro Ser Pro Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser	
645 650 655	
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Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala	
660 665 670	
gga aaa gga gtc ata gaa cag aca gaa aaa tct cat cca aga agc cct	2064
Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro	
675 680 685	
aac gtg tta tct gtc gct ttg agt caa aga act aca gtt cct gag gaa	2112
Asn Val Leu Ser Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu	
690 695 700	
gaa cta aat cca aag ata cta gct ttg cag aat gct cag aga aag cga	2160
Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg	
705 710 715 720	
aaa atg gaa cat gat ggt tca ctt ttt caa gca gta gga att gga aca	2208
Lys Met Glu His Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr	
725 730 735	
tta tta cag cag cca gac gat cat gca gct act aca tca ctt tct tgg	2256
Leu Leu Gln Gln Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp	
740 745 750	

0902258 080701

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Thr	Phe	Leu	Ser	Arg	His	Ser	Leu	Asp	Met	Lys	Phe	Ser	Tyr	Cys	Asp
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Arg	Ser	Ile	Tyr	Glu	Tyr	Tyr	His	Ala	Leu	Asp	Ser	Asp	His	Leu	Thr
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Lys	Thr	His	His	Asp	Met	Phe	Thr	Lys	Gly	Gln	Val	Thr	Thr	Gly	Gln
	290					295					300				
Tyr	Arg	Met	Leu	Ala	Lys	Arg	Gly	Gly	Tyr	Val	Trp	Val	Glu	Thr	Gln
305					310					315					320
Ala	Thr	Val	Ile	Tyr	Asn	Thr	Lys	Asn	Ser	Gln	Pro	Gln	Cys	Ile	Val
				325					330					335	
Cys	Val	Asn	Tyr	Val	Val	Ser	Gly	Ile	Ile	Gln	His	Asp	Leu	Ile	Phe
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Ser	Leu	Gln	Gln	Thr	Glu	Cys	Val	Leu	Lys	Pro	Val	Glu	Ser	Ser	Asp
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Met	Lys	Met	Thr	Gln	Leu	Phe	Thr	Lys	Val	Glu	Ser	Glu	Asp	Thr	Ser
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Ser Leu Phe Asp Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu
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Ala Pro Ala Ala Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asn
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Asp Thr Glu Thr Asp Asp Gln Gln Leu Glu Glu Val Pro Leu Tyr Asn
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Asp Val Met Leu Pro Ser Pro Asn Glu Lys Leu Gln Asn Ile Asn Leu
435 440 445

Ala Met Ser Pro Leu Pro Thr Ala Glu Thr Pro Lys Pro Leu Arg Ser
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Ser Ala Asp Pro Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Pro
465 470 475 480

Asn Pro Glu Ser Leu Glu Leu Ser Phe Thr Met Pro Gln Ile Gln Asp
485 490 495

Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu
500 505 510

Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val
515 520 525

Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr
530 535 540

Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu
545 550 555 560

Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser
565 570 575

Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser
580 585 590

Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln
595 600 605

Glu Pro Thr Ala Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu
610 615 620

Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala
625 630 635 640

Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu Met Leu Ala
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 HindIII and Bst98I restriction site

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 HindIII and Bst98I restriction site

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